

RAW SEQUENCE LISTING

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Application Serial Number: 10/591,428A
Source: FWP
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RAW SEQUENCE LISTING

DATE: 04/16/2007

PATENT APPLICATION: US/10/591,428A

TIME: 19:09:03

Input Set : E:\SEQUENCE LISTING PCT.EP.2005.002449 (65084.21).txt

Output Set: N:\CRF4\04162007\J591428A.raw

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3 <110> APPLICANT: Frohberg, Claus
4      Koetting, Oliver
5      Ritte, Gerhard
6      Steup, Martin
8 <120> TITLE OF INVENTION: Plants with increased activity of a starch phosphorylating
enzyme
10 <130> FILE REFERENCE: 65085.000021
12 <140> CURRENT APPLICATION NUMBER: 10/591,428A
13 <141> CURRENT FILING DATE: 2006-09-01
15 <150> PRIOR APPLICATION NUMBER: EP04090086.2
16 <151> PRIOR FILING DATE: 2004-03-05
18 <150> PRIOR APPLICATION NUMBER: EP04090121.7
19 <151> PRIOR FILING DATE: 2004-03-29
21 <150> PRIOR APPLICATION NUMBER: US 60/549,945
22 <151> PRIOR FILING DATE: 2004-03-05
24 <160> NUMBER OF SEQ ID NOS: 25
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 3591
29 <212> TYPE: DNA
30 <213> ORGANISM: Arabidopsis thaliana
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(3591)
35 <223> OTHER INFORMATION:
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42 act aga aac tca tca tca tca ctt cct aga ctc gtt aac atc act cac      96
43 Thr Arg Asn Ser Ser Ser Ser Leu Pro Arg Leu Val Asn Ile Thr His
44          20          25          30
46 aga gtt aat ctc agc cac caa tct cac cga ctc aga aac tcc aat tct      144
47 Arg Val Asn Leu Ser His Gln Ser His Arg Leu Arg Asn Ser Asn Ser
48          35          40          45
50 cgt ctc act tgc act gct act tct tct tcc acc att gag gaa caa cgg      192
51 Arg Leu Thr Cys Thr Ala Thr Ser Ser Ser Thr Ile Glu Glu Gln Arg
52          50          55          60
54 aag aag aaa gat gga tca gga acg aaa gtg agg ttg aat gtg agg tta      240
55 Lys Lys Lys Asp Gly Ser Gly Thr Lys Val Arg Leu Asn Val Arg Leu
56 65          70          75          80
58 gat cat caa gtt aat ttt ggt gac cat gtg gct atg ttt gga tca gct      288
59 Asp His Gln Val Asn Phe Gly Asp His Val Ala Met Phe Gly Ser Ala
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63	Lys	Glu	Ile	Gly	Ser	Trp	Lys	Lys	Lys	Ser	Pro	Leu	Asn	Trp	Ser	Glu	
64				100					105				110				
66	aat	gga	tgg	gtt	tgt	gag	ttg	gaa	ctt	gac	ggt	ggt	cag	gtt	ttg	gag	384
67	Asn	Gly	Trp	Val	Cys	Glu	Leu	Glu	Leu	Asp	Gly	Gly	Gln	Val	Leu	Glu	
68			115					120					125				
70	tat	aag	ttt	gtc	att	gtt	aag	aat	gat	ggt	tca	ctt	tca	tgg	gaa	tct	432
71	Tyr	Lys	Phe	Val	Ile	Val	Lys	Asn	Asp	Gly	Ser	Leu	Ser	Trp	Glu	Ser	
72		130					135					140					
74	ggt	gat	aat	cgt	gtc	ctt	aag	gtt	cca	aat	tct	ggg	aat	ttt	tct	gtt	480
75	Gly	Asp	Asn	Arg	Val	Leu	Lys	Val	Pro	Asn	Ser	Gly	Asn	Phe	Ser	Val	
76	145					150				155						160	
78	gtt	tgt	cat	tgg	gat	gct	act	aga	gaa	acc	ctt	gat	ttg	cct	cag	gag	528
79	Val	Cys	His	Trp	Asp	Ala	Thr	Arg	Glu	Thr	Leu	Asp	Leu	Pro	Gln	Glu	
80				165						170				175			
82	gtt	ggt	aat	gat	gat	gat	gtt	ggt	gat	ggt	ggg	cat	gag	agg	gat	aat	576
83	Val	Gly	Asn	Asp	Asp	Asp	Val	Gly	Asp	Gly	Gly	His	Glu	Arg	Asp	Asn	
84			180					185				190					
86	cat	gat	gtt	ggt	gat	gat	aga	gta	gtg	gga	agt	gaa	aat	ggt	gcg	cag	624
87	His	Asp	Val	Gly	Asp	Asp	Arg	Val	Val	Gly	Ser	Glu	Asn	Gly	Ala	Gln	
88		195					200					205					
90	ctt	cag	aag	agt	aca	ttg	ggt	ggg	caa	tgg	caa	ggt	aaa	gat	gcg	tcc	672
91	Leu	Gln	Lys	Ser	Thr	Leu	Gly	Gly	Gln	Trp	Gln	Gly	Lys	Asp	Ala	Ser	
92		210				215					220						
94	ttt	atg	cgt	tct	aat	gat	cat	ggt	aac	aga	gaa	gtt	ggt	aga	aat	tgg	720
95	Phe	Met	Arg	Ser	Asn	Asp	His	Gly	Asn	Arg	Glu	Val	Gly	Arg	Asn	Trp	
96	225				230					235					240		
98	gat	act	agt	ggt	ctt	gaa	ggc	aca	gct	ctt	aag	atg	gtt	gag	ggt	gat	768
99	Asp	Thr	Ser	Gly	Leu	Glu	Gly	Thr	Ala	Leu	Lys	Met	Val	Glu	Gly	Asp	
100				245				250				255					
102	cgc	aac	tct	aag	aac	tgg	tgg	aga	aag	ctt	gaa	atg	gta	cgc	gag	gtt	816
103	Arg	Asn	Ser	Lys	Asn	Trp	Trp	Arg	Lys	Leu	Glu	Met	Val	Arg	Glu	Val	
104			260					265				270					
106	ata	gtt	ggg	agt	gtt	gag	agg	gag	gaa	cga	ttg	aag	gcg	ctc	ata	tac	864
107	Ile	Val	Gly	Ser	Val	Glu	Arg	Glu	Glu	Arg	Leu	Lys	Ala	Leu	Ile	Tyr	
108		275					280					285					
110	tct	gca	att	tat	ttg	aag	tgg	ata	aac	aca	ggt	cag	att	cct	tgt	ttt	912
111	Ser	Ala	Ile	Tyr	Leu	Lys	Trp	Ile	Asn	Thr	Gly	Gln	Ile	Pro	Cys	Phe	
112		290				295					300						
114	gaa	gat	gga	ggg	cat	cac	cgt	cca	aac	agg	cat	gcc	gag	att	tcc	aga	960
115	Glu	Asp	Gly	Gly	His	His	Arg	Pro	Asn	Arg	His	Ala	Glu	Ile	Ser	Arg	
116	305				310					315					320		
118	ctt	ata	ttc	cgt	gag	ttg	gag	cac	att	tgc	agt	aag	aaa	gat	gct	act	1008
119	Leu	Ile	Phe	Arg	Glu	Leu	Glu	His	Ile	Cys	Ser	Lys	Lys	Asp	Ala	Thr	
120			325					330				335					
122	cca	gag	gaa	gtg	ctt	gtt	gct	cgg	aaa	atc	cat	ccg	tgt	tta	cct	tct	1056
123	Pro	Glu	Glu	Val	Leu	Val	Ala	Arg	Lys	Ile	His	Pro	Cys	Leu	Pro	Ser	
124			340					345				350					
126	ttc	aaa	gca	gag	ttt	act	gca	gct	gtc	cct	cta	act	cgg	att	agg	gac	1104

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131 Ile Ala His Arg Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys
132      370                      375                      380
134 cat acg ata caa aat aag ctt cac cgg aat gct ggt cca gaa gat cta      1200
135 His Thr Ile Gln Asn Lys Leu His Arg Asn Ala Gly Pro Glu Asp Leu
136 385                      390                      395                      400
138 att gca aca gaa gca atg ctt caa cga att acc gag acc cca gga aaa      1248
139 Ile Ala Thr Glu Ala Met Leu Gln Arg Ile Thr Glu Thr Pro Gly Lys
140          405                      410                      415
142 tat agt gga gac ttt gtg gag cag ttt aaa ata ttc cat aat gag ctt      1296
143 Tyr Ser Gly Asp Phe Val Glu Gln Phe Lys Ile Phe His Asn Glu Leu
144          420                      425                      430
146 aaa gat ttc ttt aat gct gga agt ctc act gaa cag ctt gat tct atg      1344
147 Lys Asp Phe Phe Asn Ala Gly Ser Leu Thr Glu Gln Leu Asp Ser Met
148      435                      440                      445
150 aaa att tct atg gat gat aga ggt ctt tct gcg ctc aat ttg ttt ttt      1392
151 Lys Ile Ser Met Asp Asp Arg Gly Leu Ser Ala Leu Asn Leu Phe Phe
152      450                      455                      460
154 gaa tgt aaa aag cgc ctt gac aca tca gga gaa tca agc aat gtt ttg      1440
155 Glu Cys Lys Lys Arg Leu Asp Thr Ser Gly Glu Ser Ser Asn Val Leu
156 465                      470                      475                      480
158 gag ttg att aaa acc atg cat tct cta gct tct tta aga gaa aca att      1488
159 Glu Leu Ile Lys Thr Met His Ser Leu Ala Ser Leu Arg Glu Thr Ile
160          485                      490                      495
162 ata aag gaa ctt aat agc ggc ttg cga aat gat gct cct gat act gcc      1536
163 Ile Lys Glu Leu Asn Ser Gly Leu Arg Asn Asp Ala Pro Asp Thr Ala
164          500                      505                      510
166 att gca atg cgc cag aag tgg cgc ctt tgt gag atc ggc ctc gag gac      1584
167 Ile Ala Met Arg Gln Lys Trp Arg Leu Cys Glu Ile Gly Leu Glu Asp
168          515                      520                      525
170 tac ttt ttt gtt cta cta agc aga ttc ctc aat gct ctt gaa act atg      1632
171 Tyr Phe Phe Val Leu Leu Ser Arg Phe Leu Asn Ala Leu Glu Thr Met
172      530                      535                      540
174 gga gga gct gat caa ctg gca aaa gat gtg gga tca aga aac gtt gcc      1680
175 Gly Gly Ala Asp Gln Leu Ala Lys Asp Val Gly Ser Arg Asn Val Ala
176 545                      550                      555                      560
178 tca tgg aat gat cca cta gat gct ttg gtg ttg ggt gtt cac caa gta      1728
179 Ser Trp Asn Asp Pro Leu Asp Ala Leu Val Leu Gly Val His Gln Val
180          565                      570                      575
182 ggt cta tct ggt tgg aag caa gaa gaa tgt tta gcc att gga aat gaa      1776
183 Gly Leu Ser Gly Trp Lys Gln Glu Glu Cys Leu Ala Ile Gly Asn Glu
184          580                      585                      590
186 ctc ctt gct tgg cga gaa agg gac cta ctt gaa aaa gaa ggg gaa gag      1824
187 Leu Leu Ala Trp Arg Glu Arg Asp Leu Leu Glu Lys Glu Gly Glu Glu
188          595                      600                      605
190 gat gga aaa aca att tgg gcc atg agg ctg aaa gca act ctt gat cga      1872
191 Asp Gly Lys Thr Ile Trp Ala Met Arg Leu Lys Ala Thr Leu Asp Arg

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194	gca cgc aga tta aca gca gaa tat tct gat ttg ctt ctt caa ata ttt	1920		
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196	625	630	635	640
198	cct cct aat gtg gag att tta gga aaa gct cta gga att cca gag aat	1968		
199	Pro Pro Asn Val Glu Ile Leu Gly Lys Ala Leu Gly Ile Pro Glu Asn			
200		645	650	655
202	agt gtc aag acc tat aca gaa gca gag att cgt gct gga att att ttc	2016		
203	Ser Val Lys Thr Tyr Thr Glu Ala Glu Ile Arg Ala Gly Ile Ile Phe			
204		660	665	670
206	cag atc tca aag ctc tgc act gtt ctt cta aaa gct gta aga aat tca	2064		
207	Gln Ile Ser Lys Leu Cys Thr Val Leu Leu Lys Ala Val Arg Asn Ser			
208		675	680	685
210	ctt ggt tct gag ggc tgg gat gtc gtt gta cct gga tcg acg tct ggg	2112		
211	Leu Gly Ser Glu Gly Trp Asp Val Val Val Pro Gly Ser Thr Ser Gly			
212		690	695	700
214	aca tta gtt cag gtt gag agc att gtt ccg gga tca ttg cca gca act	2160		
215	Thr Leu Val Gln Val Glu Ser Ile Val Pro Gly Ser Leu Pro Ala Thr			
216	705	710	715	720
218	tct ggt ggt cct att att ctc ttg gtc aat aaa gct gat ggc gat gaa	2208		
219	Ser Gly Gly Pro Ile Ile Leu Leu Val Asn Lys Ala Asp Gly Asp Glu			
220		725	730	735
222	gag gta agt gct gct aat ggg aac ata gct gga gtc atg ctt ctg cag	2256		
223	Glu Val Ser Ala Ala Asn Gly Asn Ile Ala Gly Val Met Leu Leu Gln			
224		740	745	750
226	gag ctg cct cac ttg tct cac ctt ggc gtt aga gcg cgg cag gag aaa	2304		
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230	att gtc ttt gtg aca tgt gat gat gat gac aag gtt gct gat ata cga	2352		
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234	cga ctt gtg gga aaa ttt gtg agg ttg gaa gca tct cca agt cat gtg	2400		
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238	aat ctg ata ctt tca act gag ggt agg agt cgc act tcc aaa tcc agt	2448		
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240		805	810	815
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243	Ala Thr Lys Lys Thr Asp Lys Asn Ser Leu Ser Lys Lys Lys Thr Asp			
244		820	825	830
246	aag aag agc tta tct atc gat gat gaa gaa tca aag cct ggt tcc tca	2544		
247	Lys Lys Ser Leu Ser Ile Asp Asp Glu Glu Ser Lys Pro Gly Ser Ser			
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250	tct tcc aat agc ctc ctt tac tct tcc aag gat atc cct agt gga gga	2592		
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263	His Ser Glu His Gly Val Pro Ala Ser Phe Lys Val Pro Thr Gly Val	
264	900 905 910	
266	gtc ata cct ttt gga tgc atg gaa tta gct tta aag caa aat aat tgc	2784
267	Val Ile Pro Phe Gly Ser Met Glu Leu Ala Leu Lys Gln Asn Asn Ser	
268	915 920 925	
270	gaa gaa aag ttt gcg tct ttg cta gaa aaa cta gaa acc gcc aga cct	2832
271	Glu Glu Lys Phe Ala Ser Leu Leu Glu Lys Leu Glu Thr Ala Arg Pro	
272	930 935 940	
274	gag ggt ggt gag cta gac gac ata tgt gac cag atc cat gaa gtg atg	2880
275	Glu Gly Gly Glu Leu Asp Asp Ile Cys Asp Gln Ile His Glu Val Met	
276	945 950 955 960	
278	aaa acg ttg caa gtg cct aaa gaa aca atc aac agc ata agc aaa gcg	2928
279	Lys Thr Leu Gln Val Pro Lys Glu Thr Ile Asn Ser Ile Ser Lys Ala	
280	965 970 975	
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290	gtg agt ccc tgc gat cct ttg gtg ttt tca gat tgc gtt tgc caa	3069
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294	gtt tgg gct tct ctc tac aca aga aga gct gtt cta agc cgt aga	3114
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296	1025 1030 1035	
298	gct gct ggt gtc tct caa aga gaa gct tca atg gct gtt ctc gtt	3159
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302	caa gaa atg ctt tgc ccg gac tta tca ttc gtt ctg cac aca gtg	3204
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304	1055 1060 1065	
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308	1070 1075 1080	
310	cct ggt tta ggt gag act tta gct tca gga aca aga gga aca cca	3294
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314	tgg aga ctc gct tgc ggt aag ctc gac ggg att gta caa acc tta	3339
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318	gct ttc gca aac ttc agc gaa gag ctt ctt gtg tca gga aca ggt	3384
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VERIFICATION SUMMARY

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